



#10/B

SEQUENCE LISTING

<110> Stewart, A. F.
Zhang, Y.
Hallet, B.

<120> A New Tyrosine Recombinase for Genetic Engineering

<130> 9882-012-999

<140> 09/895,435
<141> 2001-06-30

<160> 10

<170> PatentIn version 3.0

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<212> DNA
<213> Bacillus thuringiensis

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caatattaat tgtgttgtat taggtgttat aataaaatata aatctagggg tttaacgcaa 180
cacaatttat cgataaataa atacttttag acgcaacaca atttataagac gcgaggaaa 240
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<213> Bacillus thuringiensis

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<213> Bacillus thuringiensis

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cacaatatta attgtgttgtt attaggtgtt ataataaata taaatctagg ggtttaacgc 180
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acc gag aac act gtt cag gga tac aca tca ggt att aga cag tac ata	96
Thr Glu Asn Thr Val Gln Gly Tyr Thr Ser Gly Ile Arg Gln Tyr Ile	
20 25 30	
aaa tgg ttt gaa ggt tcc tat gac aga aaa ttg aca aaa ttg tac cga	144
Lys Trp Phe Glu Gly Ser Tyr Asp Arg Lys Leu Thr Lys Leu Tyr Arg	
35 40 45	
caa aat atc tta gag tac att agt tat tta aag aat gtc aaa atg ttg	192
Gln Asn Ile Leu Glu Tyr Ile Ser Tyr Leu Lys Asn Val Lys Met Leu	
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aac gcc aag tcc att aac cac aag att agt agc ctt gct aaa ttt aat	240
Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu Ala Lys Phe Asn	
65 70 75 80	
gaa ttt cta ata cag aaa gga agt caa caa gat caa gta att tta tta	288
Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu Leu	
85 90 95	
gat gta aaa aag ttt tta caa agt gtg tta gag gat aat aac aaa cgt	336
Asp Val Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg	
100 105 110	
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Asn Tyr Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser	
115 120 125	
gag gca tta tct atc aaa atg aat gac ttc aat tta cag act ggg gaa	432
Glu Ala Leu Ser Ile Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu	
130 135 140	
tgt att att cga agt gga aaa gga ggt aaa caa cga att gta tta cta	480
Cys Ile Ile Arg Ser Gly Lys Gly Lys Gln Arg Ile Val Leu Leu	
145 150 155 160	
aat agt aag gta ctt agt gct atc aaa gat tat ctc atc gat cga aaa	528
Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr Leu Ile Asp Arg Lys	
165 170 175	
aca tac agt aca gca cat gaa tct ccg tat ctt ttt att agt aaa aag	576
Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser Lys Lys	
180 185 190	
cga gaa aag ctc gac cgt acg gtc gtc aat cgt atc ttt aaa tca tac	624
Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr	
195 200 205	
agg aat gtt att act cca cac caa tta cga cac ttc ttc tgt acg aat	672
Arg Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn	
210 215 220	
gca att caa aaa gga ttt agc att cat gaa gtt gca aat caa gct ggg	720
Ala Ile Gln Lys Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly	
225 230 235 240	
cac tct aac atc cat acg aca cta ctt tac aca aat cca aac caa ctg	768
His Ser Asn Ile His Thr Thr Leu Leu Tyr Thr Asn Pro Asn Gln Leu	
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 35 40 45

Gln Asn Ile Leu Glu Tyr Ile Ser Tyr Leu Lys Asn Val Lys Met Leu
 50 55 60

Asn Ala Lys Ser Ile Asn His Lys Ile Ser Ser Leu Ala Lys Phe Asn
 65 70 75 80

Glu Phe Leu Ile Gln Lys Gly Ser Gln Gln Asp Gln Val Ile Leu Leu
 85 90 95

Asp Val Lys Lys Phe Leu Gln Ser Val Leu Glu Asp Asn Asn Lys Arg
 100 105 110

Asn Tyr Ala Ile Ala Thr Leu Leu Ala Tyr Thr Gly Val Arg Ile Ser
 115 120 125

Glu Ala Leu Ser Ile Lys Met Asn Asp Phe Asn Leu Gln Thr Gly Glu
 130 135 140

Cys Ile Ile Arg Ser Gly Lys Gly Lys Gln Arg Ile Val Leu Leu
 145 150 155 160

Asn Ser Lys Val Leu Ser Ala Ile Lys Asp Tyr Leu Ile Asp Arg Lys
 165 170 175

Thr Tyr Ser Thr Ala His Glu Ser Pro Tyr Leu Phe Ile Ser Lys Lys
 180 185 190

Arg Glu Lys Leu Asp Arg Thr Val Val Asn Arg Ile Phe Lys Ser Tyr
 195 200 205

Arg Asn Val Ile Thr Pro His Gln Leu Arg His Phe Phe Cys Thr Asn
 210 215 220

Ala Ile Gln Lys Gly Phe Ser Ile His Glu Val Ala Asn Gln Ala Gly
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His Ser Asn Ile His Thr Thr Leu Leu Tyr Thr Asn Pro Asn Gln Leu
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<222> 81 .. 100
<223> n = a, t, g, or c

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ttta                                         124

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